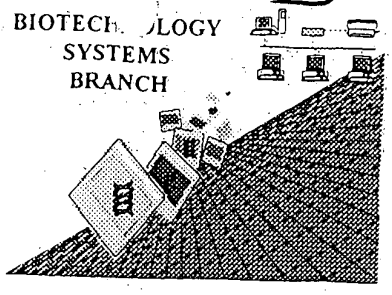
1-3

~~0330~~

#4

BIOTECH. LOGY SYSTEMS BRANCH



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/659,737

Source: OIPE

Date Processed by STIC: 2-16-01

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

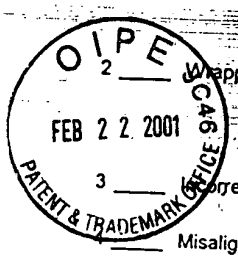
http://www.uspto.gov/web/offices/pac/checker

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/659,737

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE



1 ____ Wrapped Nucleics
The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 ____ Wrapped Aminos
The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 ____ Incorrect Line Length
The rules require that a line not exceed 72 characters in length. This includes spaces.

____ Misaligned Amino Acid Numbering
The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 ____ Non-ASCII
This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 ____ Variable Length
Sequence(s) ____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.

7 ____ PatentIn ver. 2.0 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

8 ____ Skipped Sequences (OLD RULES)
Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 ____ Skipped Sequences (NEW RULES)
Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

10 ✓ Use of n's or Xaa's (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 ____ Use of <213>Organism (NEW RULES)
Sequence(s) _____ are missing this mandatory field or its response.

12 ____ Use of <220>Feature (NEW RULES)
Sequence(s) ____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)

13 ____ PatentIn ver. 2.0 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/659,737

DATE: 02/16/2001
TIME: 11:33:38

Input Set : A:\10489a1.app
Output Set: N:\CRF3\02162001\I659737.raw

Does Not Comply
Corrected Diskette Needed
See p. 6

```
      3 <110> APPLICANT: Blumenberg, Miroslav
      4       Gazel, Alix M
      6 <120> TITLE OF INVENTION: GENES AND POLYNUCLEOTIDES ASSOCIATED WITH ULTRAVIOLET
      7       RADIATION-MEDIATED SKIN DAMAGE AND USES THEREOF
      9 <130> FILE REFERENCE: PC10489A
C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/659,737
C--> 12 <141> CURRENT FILING DATE: 2000-09-11
     14 <150> PRIOR APPLICATION NUMBER: 60/155,029
     15 <151> PRIOR FILING DATE: 1999-09-20
     17 <160> NUMBER OF SEQ ID NOS: 19
     19 <170> SOFTWARE: PatentIn Ver. 2.1
     21 <210> SEQ ID NO: 1
     22 <211> LENGTH: 164
     23 <212> TYPE: DNA
     24 <213> ORGANISM: Homo sapiens
     26 <220> FEATURE:
     27 <221> NAME/KEY: CDS
     28 <222> LOCATION: (2)..(163)
     30 <400> SEQUENCE: 1
     31 g cac cgg gac atc aag gca gga aat att ttg cta ctt gag aag ata gaa 49
     32   His Arg Asp Ile Lys Ala Gly Asn Ile Leu Leu Leu Glu Lys Ile Glu
     33     1               5                  10                  15
     35 cat gat gac atc tgc aat aaa act ttg aag att aca gat ttt ggg ttg   97
     36 His Asp Asp Ile Cys Asn Lys Thr Leu Lys Ile Thr Asp Phe Gly Leu
     37                 20                  25                  30
     39 gcg agg gaa tgg cac agg acc acc aaa atg agc aca gca ggc acc tat   145
     40 Ala Arg Glu Trp His Arg Thr Thr Lys Met Ser Thr Ala Gly Thr Tyr
     41          35                  40                  45
     43 gcc tgg atg gcc cca gaa g                                       164
     44 Ala Trp Met Ala Pro Glu
     45       50
     48 <210> SEQ ID NO: 2
     49 <211> LENGTH: 54
     50 <212> TYPE: PRT
     51 <213> ORGANISM: Homo sapiens
     53 <400> SEQUENCE: 2
     54 His Arg Asp Ile Lys Ala Gly Asn Ile Leu Leu Leu Glu Lys Ile Glu
     55   1               5                  10                  15
     57 His Asp Asp Ile Cys Asn Lys Thr Leu Lys Ile Thr Asp Phe Gly Leu
     58                 20                  25                  30
     60 Ala Arg Glu Trp His Arg Thr Thr Lys Met Ser Thr Ala Gly Thr Tyr
     61          35                  40                  45
     63 Ala Trp Met Ala Pro Glu
     64       50
     68 <210> SEQ ID NO: 3
     69 <211> LENGTH: 145
     70 <212> TYPE: DNA
```

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/659,737

DATE: 02/16/2001
TIME: 11:33:38

Input Set : A:\10489a1.app
Output Set: N:\CRF3\02162001\I659737.raw

```
 71 <213> ORGANISM: Homo sapiens
 73 <220> FEATURE:
 74 <221> NAME/KEY: CDS
 75 <222> LOCATION: (2)..(145)
 77 <400> SEQUENCE: 3
 78 a\cat cgg gac atc aag agc gac tcg atc ctg ctg acc cat gat ggc agg 49
 79   His Arg Asp Ile Lys Ser Asp Ser Ile Leu Leu Thr His Asp Gly Arg
 80     1               5                  10                  15
 82 gtg aag ctg tca gac ttt ggg ttc tgc gcc cag gtg agc aag gaa gtg   97
 83 Val Lys Leu Ser Asp Phe Gly Phe Cys Ala Gln Val Ser Lys Glu Val
 84             20                  25                  30
 86 ccc cga agg aag tcg ctg gtc ggc acg ccc tac tgg atg gcc cca gag´ 145
 87 Pro Arg Arg Lys Ser Leu Val Gly Thr Pro Tyr Trp Met Ala Pro Glu
 88         35                  40                  45
 91 <210> SEQ ID NO: 4
 92 <211> LENGTH: 48
 93 <212> TYPE: PRT
 94 <213> ORGANISM: Homo sapiens
 96 <400> SEQUENCE: 4
 97 His Arg Asp Ile Lys Ser Asp Ser Ile Leu Leu Thr His Asp Gly Arg
 98   1               5                  10                  15
100 Val Lys Leu Ser Asp Phe Gly Phe Cys Ala Gln Val Ser Lys Glu Val
101             20                  25                  30
103 Pro Arg Arg Lys Ser Leu Val Gly Thr Pro Tyr Trp Met Ala Pro Glu
104         35                  40                  45
108 <210> SEQ ID NO: 5
109 <211> LENGTH: 146
110 <212> TYPE: DNA
111 <213> ORGANISM: Homo sapiens
113 <220> FEATURE:
114 <221> NAME/KEY: CDS
115 <222> LOCATION: (2)..(145)
117 <400> SEQUENCE: 5
118 t\cac agg gac atc aag agt gac tcc atc ctg ctg acc ctc gat ggc agg 49
119   His Arg Asp Ile Lys Ser Asp Ser Ile Leu Leu Thr Leu Asp Gly Arg
120     1               5                  10                  15
122 gtg aag ctc tcg gac ttc gga ttc tgt gct cag atc agc aaa gac gtc   97
123 Val Lys Leu Ser Asp Phe Gly Phe Cys Ala Gln Ile Ser Lys Asp Val
124             20                  25                  30
126 cct aag agg aag tcc ctg gtg gga acc ccc tac tgg atg gcg ccc gag´g 146
127 Pro Lys Arg Lys Ser Leu Val Gly Thr Pro Tyr Trp Met Ala Pro Glu
128         35                  40                  45
131 <210> SEQ ID NO: 6
132 <211> LENGTH: 48
133 <212> TYPE: PRT
134 <213> ORGANISM: Homo sapiens
136 <400> SEQUENCE: 6
137 His Arg Asp Ile Lys Ser Asp Ser Ile Leu Leu Thr Leu Asp Gly Arg
138   1               5                  10                  15
```

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/659,737

DATE: 02/16/2001
TIME: 11:33:38

Input Set : A:\10489a1.app
Output Set: N:\CRF3\02162001\I659737.raw

```
140 Val Lys Leu Ser Asp Phe Gly Phe Cys Ala Gln Ile Ser Lys Asp Val
141          20                  25                  30
143 Pro Lys Arg Lys Ser Leu Val Gly Thr Pro Tyr Trp Met Ala Pro Glu
144      35                  40                  45
148 <210> SEQ ID NO: 7
149 <211> LENGTH: 3627
150 <212> TYPE: DNA
151 <213> ORGANISM: Homo sapiens
153 <220> FEATURE:
154 <221> NAME/KEY: CDS
155 <222> LOCATION: (868)..(1275)
157 <220> FEATURE:
158 <221> NAME/KEY: CDS
159 <222> LOCATION: (1420)..(1553)
161 <220> FEATURE:
162 <221> NAME/KEY: CDS
163 <222> LOCATION: (1900)..(2026)
165 <220> FEATURE:
166 <221> NAME/KEY: CDS
167 <222> LOCATION: (2105)..(2230)
169 <220> FEATURE:
170 <221> NAME/KEY: CDS
171 <222> LOCATION: (2696)..(2833)
173 <400> SEQUENCE: 7
174 gatctgcgac ctccttcaga acctgccaaa atgactagga aaaatgctgt ttccatagca 60
176 agagccaaaa gagaacatga cggccctgca ctccgggatc tctctggcac cagattccca 120
178 gcccagggga gacacctgaa ccccccagat ggtgacacac ctctgtggtc ctctgtcagg 180
180 gacataacct cccagcacag atttgcaaac tccctgctgc aggcacaagc agggctatcg 240
182 ggccccaggt gtggctcccc tgccttggtt cagggagtgg agacacagtt gcccactgct 300
184 ccccacccca ctgccaggcc tcttctgccc ccatgggtcc tggggtgggg gagccttggg 360
186 agttgaagaa tgcctctgac ccagattctt caagcagcct ctgagctcag aggaagagtc 420
188 tgcctcacgg cagcctccct ggggtctagc tgtcaatcgc ccaggaagaa atacccagcg 480
190 cgggacccgg cggggaagct ggccttctct gtcttcccag gtgcagcaca gcgagtgtaa 540
192 ggagctgtct tgggcctgcc cagcctggtg ccctgcgggg gactgctggc acaggactgt 600
194 gactgggctt cagctctgtc tgaaaatctt tgcttcagag cacctcccta gtttgatctg 660
196 ataccccgcc tgaccctgcc agagtccaga ggtcacggcg gccagccccc gcctccggga 720
198 aggttattcc aaatgctccc acagccctga cccttcctgt tgctttgtcc cttgcagccc 780
200 aactcctctt tccgaccgcc gcagaaagac aacccccaa gcctggtggc caaggcccag 840
202 tccttgcccc cggaccagcc ggtgggg acc ttc agc cct ctg acc act tcg gat 894
203                              Thr Phe Ser Pro Leu Thr Thr Ser Asp
204                                1               5
206 acc agc agc ccc cag aag tcc ctc cgc aca gcc ccg gcc aca ggc cag   942
207 Thr Ser Ser Pro Gln Lys Ser Leu Arg Thr Ala Pro Ala Thr Gly Gln
208  10                  15                  20                  25
210 ctt cca ggc cgg tct tcc cca gcg gga tcc ccc cgc acc tgg cac gcc   990
211 Leu Pro Gly Arg Ser Ser Pro Ala Gly Ser Pro Arg Thr Trp His Ala
212                  30                  35                  40
214 cag atc agc acc agc aac ctg tac ctg ccc cag gac ccc acg gtt gcc   1038
215 Gln Ile Ser Thr Ser Asn Leu Tyr Leu Pro Gln Asp Pro Thr Val Ala
```

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/659,737
DATE: 02/16/2001
TIME: 11:33:38

Input Set : A:\10489a1.app
Output Set: N:\CRF3\02162001\I659737.raw

```
216                 45                  50                  55
218 aag ggt gcc ctg gct ggt gag gac aca ggt gtt gtg aca cat gag cag   1086
219 Lys Gly Ala Leu Ala Gly Glu Asp Thr Gly Val Val Thr His Glu Gln
220          60                  65                  70
222 ttc aag gct gcg ctc agg atg gtg gtg gac cag ggt gac ccc cgg ctg   1134
223 Phe Lys Ala Ala Leu Arg Met Val Val Asp Gln Gly Asp Pro Arg Leu
224      75                  80                  85
226 ctg ctg gac agc tac gtg aag att ggc gag ggc tcc acc ggc atc gtc   1182
227 Leu Leu Asp Ser Tyr Val Lys Ile Gly Glu Gly Ser Thr Gly Ile Val
228  90                  95                 100                 105
230 tgc ttg gcc cgg gaa gaa cac tcg ggc cgc cag gtg gcc gtc aag atg   1230
231 Cys Leu Ala Arg Glu Glu His Ser Gly Arg Gln Val Ala Val Lys Met
232                 110                 115                 120
234 atg gac ctc aga aag cag cag cgc agg gag ctg ctc ttc aac gag /     1275
235 Met Asp Leu Arg Lys Gln Gln Arg Arg Glu Leu Leu Phe Asn Glu
236             125                 130                 135
238 gtgggaggac agggtgggac acacacgggg gcgttgggga tgggcagtga gcagccagcc 1335
240 aggctggaca tctgtgagca ggggcagtgg gtggccatgc gtctgggcac tgtgcctggc 1395
242 actcaggccc ccacctgccc ccag\gtg gtg atc atg cgg gac tac cag cac    1446
243                             Val Val Ile Met Arg Asp Tyr Gln His
244                         140                 145
246 ttc aac gtg gtg gag atg tac aag agc tac ctg gtg ggc gag gag ctg   1494
247 Phe Asn Val Val Glu Met Tyr Lys Ser Tyr Leu Val Gly Glu Glu Leu
248                 150                 155                 160
250 tgg gtg ctc atg gag ttc ctg cag gga gga gcc ctc aca gac atc gtc   1542
251 Trp Val Leu Met Glu Phe Leu Gln Gly Gly Ala Leu Thr Asp Ile Val
252             165 /               170                 175
254 tcc caa gtc ag gtgggcagct gggagggctg gaccctgagt gcaggctgcc        1593
255 Ser Gln Val Arg
256         180
258 ctcaccatgg ccctgccagg gcaatgtggt cttctgcctg tggcccagaa gacttgggat 1653
260 gcctgggctc ccctgcctgc tggggtaact gagacccagg ggtcttggga gtggagaaga 1713
262 gaaggatagc ttctagccaa agctcaggcc ccagttttca ccagggctat ggcctgactg 1773
264 tgctgccaaa cagattgcct gggagctgtg gggcctagca ccagggactc ctactctgct 1833
266 cagccacccc acgacctgcc agagctaacg ttctctttca tcgggtggcc ccaccttcct 1893
268 gtccag g ctg aat gag gag cag att gcc act gtg tgt gag gct gtg ctg   1942
269          Leu Asn Glu Glu Gln Ile Ala Thr Val Cys Glu Ala Val Leu
270                     185                 190                 195
272 cag gcc ctg gcc tac ctg cat gct cag ggt gtc atc cac cgg gac atc   1990
273 Gln Ala Leu Ala Tyr Leu His Ala Gln Gly Val Ile His Arg Asp Ile
274                 200                 205                 210
276 aag agt gac tcc atc ctg ctg acc ctc gat ggc agg / gtaggtccca      2036
277 Lys Ser Asp Ser Ile Leu Leu Thr Leu Asp Gly Arg
278             215                 220
280 tcctgtcccc ggcacagcca cgctcccact tcctcctgat ccaccactca ctccctttc 2096
282 aaccgcag\gtg aag ctc tcg gac ttc gga ttc tgt gct cag atc agc aaa  2146
283          Val Lys Leu Ser Asp Phe Gly Phe Cys Ala Gln Ile Ser Lys
284             225                 230                 235
286 gac gtc cct aag agg aag tcc ctg gtg gga acc ccc tac tgg atg gct   2194
```

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/659,737

DATE: 02/16/2001
TIME: 11:33:38

Input Set : A:\10489a1.app
Output Set: N:\CRF3\02162001\I659737.raw

```
287 Asp Val Pro Lys Arg Lys Ser Leu Val Gly Thr Pro Tyr Trp Met Ala
288         240                 245                 250
290 cct gaa gtg atc tcc agg tct ttg tat gcc act gag gtaaccgttc        2240
291 Pro Glu Val Ile Ser Arg Ser Leu Tyr Ala Thr Glu
292     255                 260                 265
294 cctccacccc ccagacctcc caaaagcaac ttggcaactg gcagctcttc tgctgtggcc 2300
296 cctccagtga gctcaccaaa agcagccctg gttttcagag tcccacctag tcaacaccct 2360
298 tccccctttc gatggggctg ctcttaccca gtgactttgc tgccaggaac gagtcctgca 2420
300 agtgctttcc tcagctcaag ggcagaatgg ggtatggccg ggcctcctat gtatgatggc 2480
302 ctttctctga gtgactgaca gctgtgtccc tataggcagt ggtcactcat gcaggcagta 2540
304 actggccaca gggcaggtga ccaggggagg aaggagacag acccaccaag gagagctggg 2600
306 gccagctgtc ccccctccac cactgctgcc accagaacgc agctaccaat gggccagggt 2660
308 ctggccatgg ggtcagggac attttcctcc tgcag gtg gat atc tgg tct ctg    2713
309                                     Val Asp Ile Trp Ser Leu
310                                                         270
312 ggg atc atg gtg att gag atg gta gat ggg gag cca ccg tac ttc agt    2761
313 Gly Ile Met Val Ile Glu Met Val Asp Gly Glu Pro Pro Tyr Phe Ser
314             275                 280                 285
316 gac tcc cca gtg caa gcc atg aag agg ctc cgg gac agc ccc cca ccc    2809
317 Asp Ser Pro Val Gln Ala Met Lys Arg Leu Arg Asp Ser Pro Pro Pro
318         290                 295                 300
320 aag ctg aaa aac tct cac aag gtc agttggcaca caagggtgcg acctcgcaga  2863
321 Lys Leu Lys Asn Ser His Lys Val
322     305                 310
324 ccccattcct cctgaggcaa ggggaccaga acctgggctc ccagcatctc ccttccactg 2923
326 aagccacagg gtctgggctc ctggaaaagg ctcctctttc cccacacaaa acccgcacct 2983
328 gggtgtggag ccgcatctac gcacaagttc gcatgtgcgc tccgacaagt cgcctcccac 3043
330 ggctgtggca ggagagttgc tgcttggcag aagggttgct gcttggcagg cactggtcgg 3103
332 aagcccagtg gggcccatga gcagggaaag ccaggacacc agcaactccc tgctgtccag 3163
334 ggagggatcc ggagaagctt cactgagcac aaacccttca acccgtgtcg ggagatccat 3223
336 accatgattc gatgtccctg tccatcacgg cgagtcggct catgctccat tcgttgcaca 3283
338 ccccgacaca gctaagccac agcgttcccc ttaaagccag tataagtgca tggaagtggt 3343
340 atacatgtaa ccctttttgc caaatcggcc ccaaccccgc aggccttact gtggacgccc 3403
342 cctgctggca ggtcagcacg gggctgataa gtggcaccgc catctggtgg ccaaaacaag 3463
344 aaatgtctca gagggctgaa gcctctcctc taaaatagca aaaaaacaag agttctgtgg 3523
346 ccccaacaca aagctggatg ggaggaccaa caggaaacat cttccaagac aactggtcct 3583
348 tggagcccgc accgctaacc ccaaaattag catataaagc atgc                  3627
351 <210> SEQ ID NO: 8
352 <211> LENGTH: 311
353 <212> TYPE: PRT
354 <213> ORGANISM: Homo sapiens
356 <400> SEQUENCE: 8
357 Thr Phe Ser Pro Leu Thr Thr Ser Asp Thr Ser Ser Pro Gln Lys Ser
358   1               5                  10                  15
360 Leu Arg Thr Ala Pro Ala Thr Gly Gln Leu Pro Gly Arg Ser Ser Pro
361             20                  25                  30
363 Ala Gly Ser Pro Arg Thr Trp His Ala Gln Ile Ser Thr Ser Asn Leu
364         35                  40                  45
366 Tyr Leu Pro Gln Asp Pro Thr Val Ala Lys Gly Ala Leu Ala Gly Glu
```

<210> 14
<211> 18
<212> DNA
<213> Homo sapiens

<400> 14
atgcamcang ayathaar

18

<210> 15
<211> 20
<212> DNA
<213> Homo sapiens

<400> 15
gcnacytcng cngccatcca

<210> 16
<211> 27
<212> DNA
<213> Homo sapiens

<400> 16
cccgaattca tgcamcanga yathaar

<210> 17
<211> 29
<212> DNA
<213> Homo sapiens

<400> 17
cccgaattcg cnacytcngg ngccatcca

29

Missing mandatory <220> to <223> features to explain the "n's" in the sequences. See #10 on the Error Summary Sheet.

Note: Though not shown, seq #11 has an "n" at position 453, which needs a <220> to <223> explanation.

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/659,737

DATE: 02/16/2001
TIME: 11:33:39

Input Set : A:\10489a1.app
Output Set: N:\CRF3\02162001\I659737.raw

L:11 M:270 C: Current Application Number differs, Replaced Application Number
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:732 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:11
L:732 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:11
L:732 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:11
L:732 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:11
L:732 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:11
L:1091 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:14
L:1091 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:14
L:1091 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:14
L:1091 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:14
L:1091 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:14
L:1100 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:15
L:1100 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:15
L:1100 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:15
L:1100 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:15
L:1100 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:15
L:1109 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:16
L:1109 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:16
L:1109 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:16
L:1109 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:16
L:1109 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:16
L:1118 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:17
L:1118 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:17
L:1118 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:17
L:1118 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:17
L:1118 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:17